


```

US-09-270-767-48563
: Sequence 48563 Application US/09/270767
: GENERAL INFORMATION:
: APPLICANT: Bombardier et al
: TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
: FILE REFERENCE: File Reference: 7326-094
: CURRENT APPLICATION NUMBER: US/09/270,767
: CURRENT FILING DATE: 1996-03-17
: NUMBER OF SEQ. ID NOS: 62517
: SOFTWARE: PatentIn Ver. 2.0
: SEQ. ID NO 48563
: TYPE: PRT
: ORGANISM: Drosophila melanogaster
US-09-270-767-48563

```

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Query Match 64.4% Score 754 DB 16 Length 204
Best Local Similarity 77.9% Pred. No. 1,5e-61
Matches 148; Conservative 20; Mismatches 22; Indels 0; Gaps 0;

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QY 23 GPTTGGVAAATPRTTQSSPEVVAHLSKRYLSEFTATPEVYDMSGLVVR 80
DB 15 EPLTSLKQVKSLELLENLQASDPTFLFLAALQVLSDFMTSVREYEHVETVDIG 74
QY 81 GPEFAATATKATVAATAFASGSHSPVVEIPKEDLSFNMGCKEONSPIYISRIIG 140
DB 75 SHDKASATATKATVAATAFASGSHAPRVVLEPKIEGLSFNMGCKEONSPIYISRIIG 134
QY 141 GVAERHGLKRGDLSVNVSVAGGHHKAVFLKAARQSVFLVYVLPKYLESEARF 200
DB 135 GVAERHGLKRGDLSVNVSVAGGHHKAVFLKAARQSVFLVYVLPKYLESEARF 194
QY 201 FKEPTAPPQ 210
DB 195 DKGNTRKKQ 204

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RESULT 15
US-09-270-8498-191322
: Sequence 191322 Application US/09/2708498
: GENERAL INFORMATION:
: APPLICANT: Swimmer et al.
: TITLE OF INVENTION: Insect genome survey devices
: FILE REFERENCE:
: CURRENT APPLICATION NUMBER: US/09/270,849B
: CURRENT FILING DATE: 1999-03-17
: NUMBER OF SEQ. ID NOS: 195450
: SOFTWARE: PatentIn Ver. 2.0
: SEQ. ID NO 191322
: LENGTH: 204
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-270-8498-191322

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```

Query Match 64.4% Score 754 DB 16 Length 204
Best Local Similarity 77.9% Pred. No. 1,5e-61
Matches 148; Conservative 20; Mismatches 22; Indels 0; Gaps 0;

```

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QY 21 GPTTGGVAAATPRTTQSSPEVVAHLSKRYLSEFTATPEVYDMSGLVVR 80
DB 15 EPLTSLKQVKSLELLENLQASDPTFLFLAALQVLSDFMTSVREYEHVETVDIG 74
QY 81 GPEFAATATKATVAATAFASGSHSPVVEIPKEDLSFNMGCKEONSPIYISRIIG 140
DB 75 SHDKASATATKATVAATAFASGSHAPRVVLEPKIEGLSFNMGCKEONSPIYISRIIG 134
QY 141 GVAERHGLKRGDLSVNVSVAGGHHKAVFLKAARQSVFLVYVLPKYLESEARF 200
DB 135 GVAERHGLKRGDLSVNVSVAGGHHKAVFLKAARQSVFLVYVLPKYLESEARF 194

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QY 201 FKEPTAPPQ 210
DB 195 DKGNTRPPQ 204

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Search completed: May 7, 2002, 12:43:57
Job time: 211 sec

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Db 126 JVALHRCSTFSTGGLSVAVSVSEBENHKAVERLKAVALVETTERVILLERLH 185
 27 201 PRTAPP 210
 Db 186 DKQNTPRP 195

RESULT 11
 US-60-191-681-13553

Sequence 13553, Application us/60191681
 GENERAL INFORMATION:
 APPLICANT: Li, Peter, W.D.
 TITLE OF INVENTION: ISOLATED DROSOPHILA PROTEINS, NUCLEIC
 TITLE OF INVENTION: ACID MOLECULES FORMING ISOLATED DROSOPHILA PROTEINS AND
 TITLE OF INVENTION: USES THEREOF
 FILE REFERENCE: C1000390
 CURRENT APPLICATION NUMBER: US/60/191,681
 CURRENT FILING DATE: 2000-03-23
 NUMBER OF SEQ ID NOS: 30973
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 13553
 LENGTH: 195
 TYPE: PRT
 ORGANISM: DROSOPHILA
 US-60-191-681-13553

Query Match 64.4% Score 754 DB 20 Length 195;
 Best Local Similarity 77.9% Pred. No. 1,4e-61;
 Matches 148; Conservative 20; Mismatches 22; Indels 0; Gaps 0;

27 21 GTTTPPVAAALELEKESGEVVRVGRKPVCEECTALEEYCYMHETTVNG 80
 DB 6 EPLTLSDVKRSTELLEKQASDPTTKIAALQVINSDFMTSVREYHIVETVLDIG 65
 27 81 CTEFPARATATVAATVAASDASHHPVVELPTEDLGTVNMGSESNPTYSPTIPG 140
 DB 66 SHIVASATATKATVAATVAASDASHHPVVELPTEDLGTVNMGSESNPTYSPTIPG 125
 QY 141 GAAHRCSTFSTGGLSVAVSVSEBENHKAVERLKAVALVETTERVILLERLH 200
 DB 126 JVALHRCSTFSTGGLSVAVSVSEBENHKAVERLKAVALVETTERVILLERLH 185
 QY 201 PRTAPP 210
 Db 186 DKQNTPRP 195

RESULT 12
 US-09-614-150-17076

Sequence 17076, Application US/09614150
 GENERAL INFORMATION:
 APPLICANT: Venter, J. Craig
 TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
 TITLE OF INVENTION: APPARATUS FOR DETECTING EXPRESSION OF 10,000 OR MORE
 FILE REFERENCE: C1000728
 CURRENT APPLICATION NUMBER: US/09/614,150
 CURRENT FILING DATE: 2000-03-11
 PRIOR APPLICATION NUMBER: 60/157,842
 PRIOR FILING DATE: 1999-10-06
 PRIOR APPLICATION NUMBER: 60/160,191
 PRIOR FILING DATE: 1999-10-19
 PRIOR APPLICATION NUMBER: 60/161,932
 PRIOR FILING DATE: 1999-10-28
 PRIOR APPLICATION NUMBER: 60/164,769
 PRIOR FILING DATE: 1999-11-12
 PRIOR APPLICATION NUMBER: 60/173,383
 PRIOR FILING DATE: 1999-12-28
 PRIOR APPLICATION NUMBER: 60/175,693
 PRIOR FILING DATE: 2000-01-12
 PRIOR APPLICATION NUMBER: 60/184,831

141 GAAHRCSTFSTGGLSVAVSVSEBENHKAVERLKAVALVETTERVILLERLH 200
 Db 126 JVALHRCSTFSTGGLSVAVSVSEBENHKAVERLKAVALVETTERVILLERLH 185
 QY 201 PRTAPP 210
 Db 186 DKQNTPRP 195

RESULT 13
 US-09-270-767-33346

Query Match 64.4% Score 754 DB 16 Length 204;
 Best Local Similarity 77.9% Pred. No. 1.5e-61;
 Matches 148; Conservative 20; Mismatches 22; Indels 0; Gaps 0;

27 21 GTTTPPVAAALELEKESGEVVRVGRKPVCEECTALEEYCYMHETTVNG 80
 DB 6 EPLTLSDVKRSTELLEKQASDPTTKIAALQVINSDFMTSVREYHIVETVLDIG 65
 QY 81 CTEFPARATATVAATVAASDASHHPVVELPTEDLGTVNMGSESNPTYSPTIPG 140
 DB 66 SHIVASATATKATVAATVAASDASHHPVVELPTEDLGTVNMGSESNPTYSPTIPG 125
 QY 141 GAAHRCSTFSTGGLSVAVSVSEBENHKAVERLKAVALVETTERVILLERLH 200
 DB 126 JVALHRCSTFSTGGLSVAVSVSEBENHKAVERLKAVALVETTERVILLERLH 185
 QY 201 PRTAPP 210
 Db 186 DKQNTPRP 195

RESULT 14
 US-09-270-767-33346

Query Match 64.4% Score 754 DB 16 Length 204;
 Best Local Similarity 77.9% Pred. No. 1.5e-61;
 Matches 148; Conservative 20; Mismatches 22; Indels 0; Gaps 0;
 27 21 GTTTPPVAAALELEKESGEVVRVGRKPVCEECTALEEYCYMHETTVNG 80
 DB 6 EPLTLSDVKRSTELLEKQASDPTTKIAALQVINSDFMTSVREYHIVETVLDIG 65
 QY 81 CTEFPARATATVAATVAASDASHHPVVELPTEDLGTVNMGSESNPTYSPTIPG 140
 DB 66 SHIVASATATKATVAATVAASDASHHPVVELPTEDLGTVNMGSESNPTYSPTIPG 125
 QY 141 GAAHRCSTFSTGGLSVAVSVSEBENHKAVERLKAVALVETTERVILLERLH 200
 DB 126 JVALHRCSTFSTGGLSVAVSVSEBENHKAVERLKAVALVETTERVILLERLH 185
 QY 201 PRTAPP 210
 Db 186 DKQNTPRP 195

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: NUMBER OF SEQ ID NOS: 745
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 369
: LENGTH: 406
: TYPE: PRT
: ORGANISM: HUMAN
US-60-229-518-369

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Query Match      67.98; Score 754; DB 24; Length 406
Best Local Similarity 82.18; Pred. No. 7.4e-65;
Matches 151; Conservative 21; Mismatches 12; Indels 0; Gaps 0;

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```

CY 28 QVAFATVETPTGCVFVPHVQSTPKVQSTFATVETVTCYMTTVERGCTTPAG 87
DB 202 DVPATVETPTGCVFVPHVQSTPKVQSTFATVETVTCYMTTVERGCTTPAG 291
CY 88 AVATATVAATVAASGSHSPVAVLPKTTGELGVNMGCKEONSPVYISPIIGGVAEHGG 147
DB 282 AVATATVAATVAASGSHSPVAVLPKTTGELGVNMGCKEONSPVYISPIIGGVAEHGG 341
CY 148 GLEGGGGLSVNVSVESEHHEKAVELLKAAKDSVKLVVVTYTPKVI PFMFAPEKELTPAP 207
DB 342 GLEGGGGLSVNVSVESEHHEKAVELLKAAKDSVKLVVVTYTPKVI PFMFAPEKELTPAP 401

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CY 208 KRQV 211
DB 402 KRQV 405

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RESULT 8
US-60-167-245-601
: Sequence 601 Affiliation US/60167245
: GENERAL INFORMATION:
: APPLICANT: LI, Peter, W.D.
: TITLE OF INVENTION: ISOLATED ION CHANNEL PROTEINS, NUCLEIC
: TITLE OF INVENTION: ACID MOLECULES ENCODING ION CHANNEL PROTEINS AND USES
: FILE REFERENCE: C1000151
: CURRENT APPLICATION NUMBER: US/60167,245
: CURRENT FILING DATE: 1999-11-24
: NUMBER OF SEQ ID NOS: 789
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 601
: LENGTH: 195
: TYPE: PRT
: ORGANISM: Drosophila
US-60-167-245-601

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Query Match      64.48; Score 754; DB 24; Length 195;
Best Local Similarity 77.98; Pred. No. 1.4e-61;
Matches 148; Conservative 20; Mismatches 22; Indels 0; Gaps 0;

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CY 21 QPTTDEPVAAVAFVETPTGCVFVPHVQSTPKVQSTFATVETVTCYMTTVERG 80
DB 6 EPTTDSKVKSTLEETLKASGDFPTTKLAALGVNMGCKEONSPVYISPIIGGVAEHGG 65
CY 81 QPFRPATAVATVAATVAASGSHSPVAVLPKTTGELGVNMGCKEONSPVYISPIIGGVAEHGG 140
DB 66 SHVPVASTATVAATVAASGSHSPVAVLPKTTGELGVNMGCKEONSPVYISPIIGGVAEHGG 125
CY 141 QVAFPHQVETPTGCVFVPHVQSTPKVQSTFATVETVTCYMTTVERGCTTPAG 200
DB 126 QVAFPHQVETPTGCVFVPHVQSTPKVQSTFATVETVTCYMTTVERGCTTPAG 185
CY 201 EKLRTAPRQ 210
DB 186 DKKRNTKRQ 195

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RESULT 9
US-60-173-463-14024

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: Sequence 14024 Affiliation US/60173464
: GENERAL INFORMATION:
: APPLICANT: LI, Peter W.D.
: TITLE OF INVENTION: ISOLATED G-PROTEIN COUPLED RECEPTORS,
: TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING GPCR PROTEINS AND USES
: FILE REFERENCE: C1000173
: CURRENT APPLICATION NUMBER: US/60173,464
: CURRENT FILING DATE: 1999-12-29
: NUMBER OF SEQ ID NOS: 30269
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 14024
: LENGTH: 195
: TYPE: PRT
: ORGANISM: Drosophila
US-60-173-463-14024

```

```

Query Match      64.48; Score 754; DB 24; Length 195;
Best Local Similarity 77.98; Pred. No. 1.4e-61;
Matches 148; Conservative 20; Mismatches 22; Indels 0; Gaps 0;

```

```

CY 21 QPTTDEPVAAVAFVETPTGCVFVPHVQSTPKVQSTFATVETVTCYMTTVERG 80
DB 6 EPTTDSKVKSTLEETLKASGDFPTTKLAALGVNMGCKEONSPVYISPIIGGVAEHGG 65
CY 81 QPFRPATAVATVAATVAASGSHSPVAVLPKTTGELGVNMGCKEONSPVYISPIIGGVAEHGG 140
DB 66 SHVPVASTATVAATVAASGSHSPVAVLPKTTGELGVNMGCKEONSPVYISPIIGGVAEHGG 125
CY 141 QVAFPHQVETPTGCVFVPHVQSTPKVQSTFATVETVTCYMTTVERGCTTPAG 200
DB 126 QVAFPHQVETPTGCVFVPHVQSTPKVQSTFATVETVTCYMTTVERGCTTPAG 185
CY 201 EKLRTAPRQ 210
DB 186 DKKRNTKRQ 195

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RESULT 10
US-60-191-637-17123
: Sequence 17123 Affiliation US/60191637
: GENERAL INFORMATION:
: APPLICANT: Venter, J. Craig
: TITLE OF INVENTION: NUCLEIC ACID DETECTOR KITS COMPRISING
: TITLE OF INVENTION: GENE SEQUENCES EXPRESSED FROM THE DROSOPHILA CHINER, AND
: TITLE OF INVENTION: USES THEREOF
: FILE REFERENCE: C1000392
: CURRENT APPLICATION NUMBER: US/60191,637
: CURRENT FILING DATE: 2000-03-23
: NUMBER OF SEQ ID NOS: 42660
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 17123
: LENGTH: 195
: TYPE: PRT
: ORGANISM: DROSOPHILA
US-60-191-637-17123

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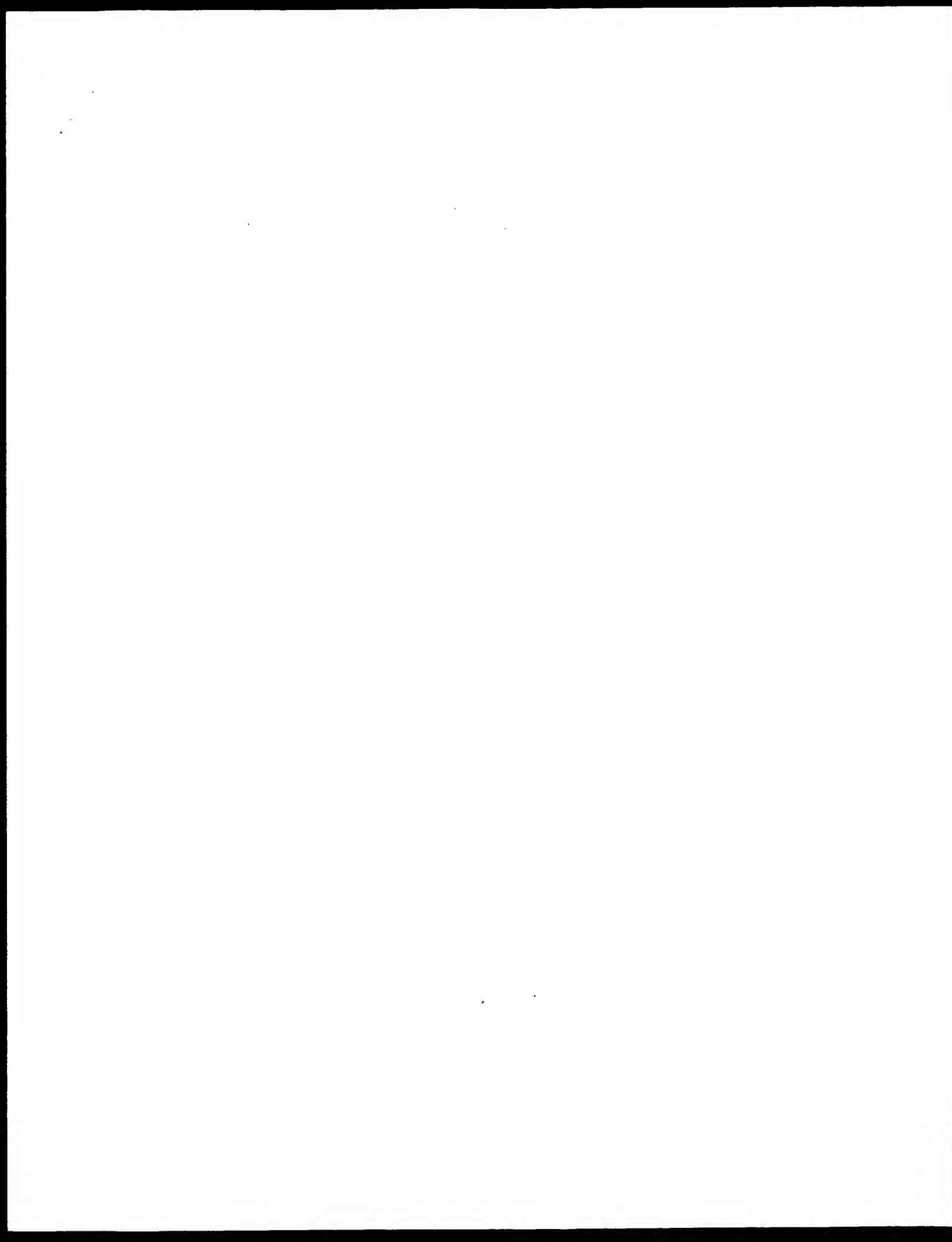
Query Match      64.48; Score 754; DB 24; Length 195;
Best Local Similarity 77.98; Pred. No. 1.4e-61;
Matches 148; Conservative 20; Mismatches 22; Indels 0; Gaps 0;

```

```

CY 21 QPTTDEPVAAVAFVETPTGCVFVPHVQSTPKVQSTFATVETVTCYMTTVERG 80
DB 6 EPTTDSKVKSTLEETLKASGDFPTTKLAALGVNMGCKEONSPVYISPIIGGVAEHGG 65
CY 81 QPFRPATAVATVAATVAASGSHSPVAVLPKTTGELGVNMGCKEONSPVYISPIIGGVAEHGG 140
DB 66 SHVPVASTATVAATVAASGSHSPVAVLPKTTGELGVNMGCKEONSPVYISPIIGGVAEHGG 125
CY 141 QVAFPHQVETPTGCVFVPHVQSTPKVQSTFATVETVTCYMTTVERGCTTPAG 200
DB 126 QVAFPHQVETPTGCVFVPHVQSTPKVQSTFATVETVTCYMTTVERGCTTPAG 185

```

PA (MWER-) MYRIAD GENETICS INT.
 XX
 PI Bartel PL, Tavligian SV;
 XX
 DR WPI: 1999-458472/38.
 DR N-PSNR: AAX86365.
 XX
 PI MMS1, an MMAC1 (tumour suppressor) interacting protein and related
 PI polynucleotides
 XX
 PS Claim 14: Page 88-93; 107pp; English
 XX
 CC The present sequence represents a MMS1 protein. The protein is a MMAC1
 CC interacting protein which is involved in tumour suppression activity
 CC in the MMAC1 pathway. MMS1, antigenic fragments or fusion proteins of
 CC these are used as immunogens for antibody production. Primers derived
 CC from MMS1 genomic clones can be used for identification of MMS1 genes
 CC and for 3'UTR tests by amplification of MMS1 RNA. RNA binding in an
 CC alteration in MMS1 can be used to diagnose cancer. A germline alteration
 CC in an MMS1 gene is indicative of a predisposition to cancer. A somatic
 CC mutation in an MMS1 gene is indicative that the tissue is neoplastic
 CC Analysis of MMAC1 and MMS1 (or PDZ domain 6 of MMS1) binding
 CC interactions can be used for detection of alterations in MMAC1
 CC associated with cancer. Wild-type MMS1 or a homologue can be used to
 CC supply wild-type MMS1 gene function for a substantially similar
 CC function) to a cell, which has lost the gene function due to a MMS1
 CC gene mutation. The gene suppresses neoplastic growth of the cell.
 CC Transgenic animals having an altered MMS1 can be used as a model for
 CC identifying drug candidates useful in treating cancer
 XX
 SU Sequence 1881 AA.
 XX
 Query Match: 16 39 Score 190, FR 20, Length 1981.
 Best Local Similarity: 25.68, Pred. No. 1.5e-03,
 Matches: 54; Conservative: 36; Mismatches: 61; Indels: 60; Gaps: 6;
 OY 31 RALELEKLQPS-----GEVVEIKSLKKEVSEFQALFEVYVMRPTD 77
 Db 1675 pvcvlorolstajstjgrgspglgdp-----limgtsgaartgplkkgdins 1729
 OY 78 VMDGP-----EPRAKATAVAANA-----SRGHS 104
 Db 1720 tngtpdajshdtrvnlknaytrillvyadnlsalaaalemslyhlsfptachp 1789
 OY 105 H-----PVEVLEPKTDELTGVNMGQ---KEQNSPIVSPTEGVAVPQICKEPQGL 156
 Db 1790 eahetfthtltlttctgssjlljststgqjvtehpdlfpjmtlclpgrahhghlcrqdt 1845
 OY 156 LSVNVSVEEHEHKAVALAKADSKIVV 186
 Db 1850 lavgqlltqqltbcgavallkkgatrttllv 1890
 RESULT 15
 AAB55834
 ID AAB55834 standard; Peptide: 344 AA.
 AC AAB55834;
 XX
 DT 07-MAR-2001 (first entry)
 XX
 DE PDZ encoded domain #4.
 XX
 KW Hematopoietic cell; FDZ; PL; autoimmune disease; inflammation;
 XX allergy; asthma; multiple sclerosis; cancer; infection.
 OS Synthetic.
 XX
 PN WO200069896-A2.
 XX
 PU 23-NOV-2000.

PE 12-MAY-2000; 2000WO-US13161.
 XX
 PR 14-MAY-1999; 990S-0134114.
 PR 14-MAY-1999; 990S-0134117.
 PR 14-MAY-1999; 990S-0134118.
 PR 21-OCT-1999; 990S-0169860.
 PR 26-OCT-1999; 990S-0163498.
 PR 13-DEC-1999; 990S-0170453.
 PR 14-JAN-2000; 2000US-0176195.
 PR 14-FEB-2000; 2000US-0182296.
 PR 11-APR-2000; 2000US-0196460.
 PR 11-APR-2000; 2000US-0196527.
 PA (APEC-) APEC VITA CORP.
 XX
 PI In PS;
 XX
 DE WPI: 2001 000-15 79.
 XX
 PT Modulating a biological function of an endothelial cell or
 PT hematopoietic cell; useful for treating autoimmune diseases and
 PT infectious diseases; by administering an antagonist that inhibits
 PT binding between a PDZ protein and a PL protein
 XX
 F3 disclosure; Page 28-43; 14pp; English.
 XX
 CC The present invention relates to a new method for modulating a
 CC biological function of an endothelial cell or hematopoietic cell. The
 CC method involves introducing into a cell, an antagonist that inhibits
 CC binding between a PDZ protein and a PL protein. The inhibitor is used
 CC to treat a disease mediated by hematopoietic cells, e.g., autoimmune
 CC disease. It may also be used to prevent transplantation rejection of
 CC a solid organ transplant. The method may also be used in the treatment
 CC of inflammation, allergy, inflammatory bowel diseases, ulcerative
 CC colitis, hepatitis, psoriasis, asthma, atopic dermatitis, autoimmune
 CC diseases (e.g., rheumatoid arthritis, multiple sclerosis,
 CC insulin-dependent diabetes, Hashimoto thyroiditis, osteoarthritis,
 CC graft rejection, transplantation rejection), atherosclerosis, cancers,
 CC infectious diseases, ischemia, vasculitis and Crohn's disease.
 XX
 SU Sequence 344 AA:
 XX
 Query Match: 15 51 Score 181.5, FR 22, Length 344;
 Best Local Similarity: 42.08, Pred. No. 9.3e-10;
 Matches: 37; Conservative: 19; Mismatches: 31; Indels: 1; Gaps: 1;
 OY 106 LTVVETLTLVSLIRWSESEVLSLTLTLGVATPESLAKSGGLASVWGSVVG 105
 Db 257 frrlvthrtstqigfahlyqg-edggcflstllaygpadlsqclfkqdgllstsvydlrn 315
 OY 166 EHEHKAVALAKADSKIVVRYTPKVL 193
 Db 316 asheqaaialkkaqgtvulliaqykpetl 343

Search completed: May 7, 2002, 12:41:21
 Job time: 116 sec

FA (REGO) UNIV CALIFORNIA.

XX Brodt DS, Brennan JE, Chao DS;

XX WJ: 1997-47055/44.

XX N-PSDM; AAT93775.

XX Diagnosing muscular dystrophy by detecting absence or decrease of
P1 neuronal nitric oxide synthase (nNOS) in skeletal muscle sarcolemma
P1 - using new nNOS binding post-synaptic density proteins, PSD-93 and
P1 PSD-95; also used for the diagnosis, prophylaxis and treatment of
P1 stroke and other neurodegenerative diseases

XX Claim 16; Page 74-76; 14pp; English.

XX This sequence is a partial sequence of post synaptic density protein-93
CC (PSD-93). PSD-93 can be used in the method of the invention for
CC diagnosing muscular dystrophy (MD) in a mammal by detecting absence or a
CC decrease of neuronal nitric oxide synthase (nNOS) in a skeletal muscle
CC sample, for pools with presence or absence of PSD-93. PSD-93 is of nNOS in
CC skeletal muscle, in addition to lack of functional dystrophin. nNOS is
CC normally targeted to the sarcolemma by associating to dystrophin (via the
CC N-terminal PDZ domain (66 aa motif bearing homology to a heptapeptide
CC family of signaling enzymes localized at cell-cell junctions) of nNOS,
CC interacting specifically with the PDZ domain of the alpha 1 syntrophin
CC component). The binding proteins PSD-93 and -95 also have a PDZ domain
CC and interact with nNOS mediating binding of nNOS to the NMDA receptor
CC located at synapses. The PSD proteins are involved in the development and
CC progression of stroke and some neurodegenerative diseases (e.g.
CC Huntington's and Alzheimer's diseases and amyotrophic lateral sclerosis).
CC so inhibiting them (or their binding) can be used to treat or, such
CC diseases (associated with overactivation of NMDA receptors) or excessive
CC levels of nNOS. This method allows early diagnosis of MD. MD can now be
CC treated by gene therapy, using only the treatment of dystrophin involved
CC in formation of the nNOS-sarcolemma/dystrophin complex, rather than the
CC complete dystrophin gene which is too large to manipulate.

XX Sequence 862 AA;

XX Query Match 16.98; Score 197.5; DB 16; Length 832;

XX Best local Similarity 44.88; Pred. No. 15; 10;

XX Matches 49; Conservative 25; Mismatches 53; Indels 15; Gaps 3;

XX 88 ATAAATVAAAPASHSHPPVVEIKKIDKQSNVMSCKKQKQVYLSKINQVAMK 147

XX 414 ATGHSYLAFAISLPPKYLKSLDILHQAQFQDQGLHSLDLAGQGLD 472

XX 119 GPRPCTGVNVEVQVPPFAVPIVAAQVVEVNVYIKVILGAGL 204

XX 473 ELDTKQLISQALIPQSLHQAIP LKATPIVLIAPYDQATVCKLHIDRPM 531

XX 205 -----TARRQQAQGLTQ 217

XX 542 NALMSQSSQSLTIRKSLYR 554

XX RESULT 14

XX AAB22148

XX AAB22138 standard; popl id: 767 AA.

XX AAB22138;

XX 21-FEB-2001 (first entry)

XX Human post-synaptic density protein 95 PSD95.

XX Human post-synaptic density protein 95; PSD-95; PDZ domain- glut loop;

XX PIP domain; muscular dystrophy.

XX Homo sapiens.

XX W020004002-A1.

XX 17-AUG-2000.

XX 09-FEB-2000; 2000W0-GH00374.

XX 09-FEB-1999; 99GB-0002696.

XX (MED1-) MEDICAL RES COUNCIL.

XX Spillanti MG, Goederl M, Hasegawa M, Huse-Schroter V, Thomas G;

XX Cohen P, Genda A;

XX WPI: 2000-55826/51.

XX Novel methods for identifying compounds useful for treating muscular
P1 dystrophy comprising identifying modulators of protein kinase and PDZ
P1 domain binding -

XX Disclosure; Fig 11, 12pp; English.

XX The present sequence is the protein sequence of the human post-synaptic
CC density protein 95 (PSD-95). It is described with reference to the
CC methods of the invention, which involve the identification of compounds
CC which are able to modulate the interaction between PDZ domains (also
CC known as PIF or GIG domains) and protein kinases. The invention also
CC comprises peptide fragments derived from stress-activated protein kinases
CC which are involved in protein phosphorylation. The compounds and peptides
CC can be used in the treatment of muscular diseases, for example muscular
CC dystrophy, or in cases where modulation of phosphorylation of proteins
CC with PDZ domains is modulation of signalling via activin receptors or
CC voltage gated channels is necessary, or in instances where the
CC localisation of SAPK3 at the neuromuscular junction or sarcolemma needs
CC to be disrupted.

XX Sequence 767 AA;

XX Query Match 16.68; Score 194.5; DB 21; Length 767;

XX Best local Similarity 41.48; Pred. No. 15; 10;

XX Matches 41; Conservative 19; Mismatches 38; Indels 1; Gaps 1;

XX 166 EAVVLLFTFEESEFNMAKQKQSLVLSKIDGVAIAPGALAKESVLAISVAVSG 166

XX 354 PRVIVPSTQGLIDVPG-SDPGHLLSLDLAGPADLSP-LRQDHLISVINDLN 412

XX 156 EHHKAVETLVAAKSVELVPTPVVLEHMAPPEKIP 204

XX 418 ASHGQALDILKALIGTLLDAPFPGVSTLADINDI 451

XX RESULT 14

XX AAY24025

XX AAY24025 standard; Protein; 1801 AA.

XX AAY24025;

XX 29-SEP-1999 (first entry)

XX Amino acid sequence of the human MMS1 protein.

XX Human MMS1 protein; MMS1 interacting protein; tumour suppressor;

XX MMS1 pathway; Immunogen; cancer; cell neoplastic growth.

XX Homo sapiens.

XX W0993656-A1.

XX 22-JUL-1999.

XX 19-JAN-1999; 99W0-0500995.

XX 20-JAN-1998; 9808-0071861.

AAV40137
 ID AAV30137 standard; Protein: 817 AA.
 XX
 AC AAV30137;
 XX
 DT 27-OCT-1999 (first entry)
 XX
 DE Amino acid sequence of tumour suppressor protein NF- κ B
 XX
 KW Nedasin, tumour suppressor protein, NF- κ B, tumour suppression
 XX
 OS Homo sapiens.
 XX
 PN WO9433702-A1.
 XX
 PD 02-SEP-1999.
 XX
 PP 24-AUG-1998; 98WO-JP03740.
 XX
 PK 25-FEB-1998; 98JP-0043552.
 XX
 PA (SUME) SUMITOMO ELECTRIC IND CO.
 XX
 PI Kishimoto T, Kuwahara H, Nawa S, Saya H,
 XX
 DR WPI: 1999-51845/73
 DP N-PSDB: AAX85725.
 XX
 PT New nedasin protein, useful in the investigation of the mechanism of
 P1 formation of malignant tumours
 XX
 PS Example 1; Page 81-87; 104pp; Japanese.
 XX
 CC The present sequence represents tumour suppressor protein NF- κ B. The
 CC specification describes mammalian proteins, designated nedasin,
 CC which bind to the tumour suppressor protein NF- κ B. Nedasin is involved
 CC with the regulation of tumour suppression mechanisms. Nedasin and
 CC antibodies recognizing it are useful in the investigation of the
 CC mechanism of formation of malignant tumours. The polynucleotides are
 CC useful for screening cDNA libraries, and as a source of primers and
 CC probes.
 XX
 SQ Sequence 817 AA;
 XX
 Query Match 17.4%; Score 203.5; DB 20; Length 817;
 Best local similarity 43.4%; Pred. No. 2e-11;
 Matches 43; Conservative 18; Mismatches 37; Indels 1; Gaps 1;
 QY 106 PAVVFLPKTTFQIGFNVWQKQNSPIYSKIPGVAFPHQKPKWLSVNSVSE3 155
 DB 384 PRLILHKGSTGYHINAGY-EDGEGITISILAGPADLSYELTIGDITISVAGNITIN 442
 QY 166 EHHKRAVPIIKAKNSVPIVVPYTPVLEMEAPFEKLR 204
 DB 443 ALHGYAALKRAQSVTLVAGYPRQYSRTSKINDIR 481
 RESULT 11
 ID AAM48102 standard; Protein: 849 AA.
 XX
 AC AAM48102;
 XX
 DT 15-JUN-1998 (first entry)
 XX
 DE Human discs large 1 gene-2 cancer related molecule.
 XX
 KW Human; NF- κ B, discs large 1 gene, cancer related molecule, nerve,
 XX
 OS Homo sapiens.

XX
 PN JP10066581-A.
 XX
 PD 10-MAR-1998.
 XX
 PK 23-AUG-1996; 96JP-0241370.
 XX
 DE 23 AUG 1996; 96JP-0241370.
 XX
 PA (SUME) SUMITOMO ELECTRIC IND CO.
 XX
 DR WPI: 1998-224339/20.
 DP N-PSDB: AAV20420.
 XX
 PT Human discs large 1 gene family - useful in, e.g. therapeutic
 P1 composition(s) for treating cancer
 XX
 PS Claim 8; Page 18 20; 31pp; Japanese.
 XX
 CC The present sequence represents human dig 2 molecule. The present
 CC invention describes human discs large 1 gene (dig) family expressible in
 CC nerve tissue. Also described are: (1) a polynucleotide (PN) encoding dig
 CC and comprising a 3100 (1) or 3213 bp (11) sequence; (2) RNA corresponding
 CC to PN having sequences (1) and (11); (3) RNA having a base sequence
 CC translated by dig; (4) an antisense PN having a at least 15 bp sequence,
 CC and which is a part of PN of (1); (5) a derivative of the antisense PN;
 CC (6) an antibody specific for dig; and (7) an antibody specific for a
 CC polypeptide having a 817 or 849 aa sequence. The polypeptide, RNA's and
 CC antibodies can be used for detection of dig. The antisense PN can be
 CC used as a therapeutic composition for treating cancer.
 XX
 SQ Sequence 849 AA;
 XX
 Query Match 17.4%; Score 203.5; DB 19; Length 849;
 Best local similarity 43.4%; Pred. No. 2.2e-11;
 Matches 43; Conservative 18; Mismatches 37; Indels 1; Gaps 1;
 QY 106 PAVVFLPKTTFQIGFNVWQKQNSPIYSKIPGVAFPHQKPKWLSVNSVSE3 155
 DB 384 PRLILHKGSTGYHINAGY-EDGEGITISILAGPADLSYELTIGDITISVAGNITIN 442
 QY 166 EHHKRAVPIIKAKNSVPIVVPYTPVLEMEAPFEKLR 204
 DB 443 ALHGYAALKRAQSVTLVAGYPRQYSRTSKINDIR 481
 RESULT 12
 ID AAM34662 standard; Protein: 882 AA.
 XX
 AC AAM34662;
 XX
 DT 29-JUN-1998 (first entry)
 XX
 DE Partial PSD-93 protein sequence.
 XX
 KW PSD 93, GINS, neuronal nitric oxide synthase, Alzheimer's disease,
 KW diagnosis, muscular dystrophy, skeletal muscle, Huntington's disease;
 KW Duchenne muscular dystrophy; Becker muscular dystrophy; dystrophin
 KW sarcoplasmic reticulum; the domain; neurodegenerative disease; gene therapy;
 KW amyotrophic lateral sclerosis.
 XX
 OS Rattus sp.
 XX
 PN WO9733173-A1.
 XX
 PD 12-SEP-1997.
 XX
 PK 05-MAR-1997; 97WO-0504897.
 XX
 PR 08-MAR-1996; 96US-0613114.

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OM protein - protein search, using SW method

Run on: May 7, 2002, 12:39:25 ; Search time 27.4 seconds

737.567 Million cell updates/sec

File:	US-09-909-005-1
Perfect Score:	120
Score:	109
1 M P S V I S A D I A M A T I V I L I C I T A T I O N T E R M I N E S 23

Scoring table: [BioSOM62](#)
Capac 10.0 , σ popt 0.5

total number of hits satisfying chosen parameters:	52245
Minimum hit seq length:	0
Maximum hit seq length:	200000000

1981-processing:	Minimum	Match 08
	Maximum	Match 100%
Listing first	45 summaries	

Database : A_tetoseq_101 : *

[illegible]

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

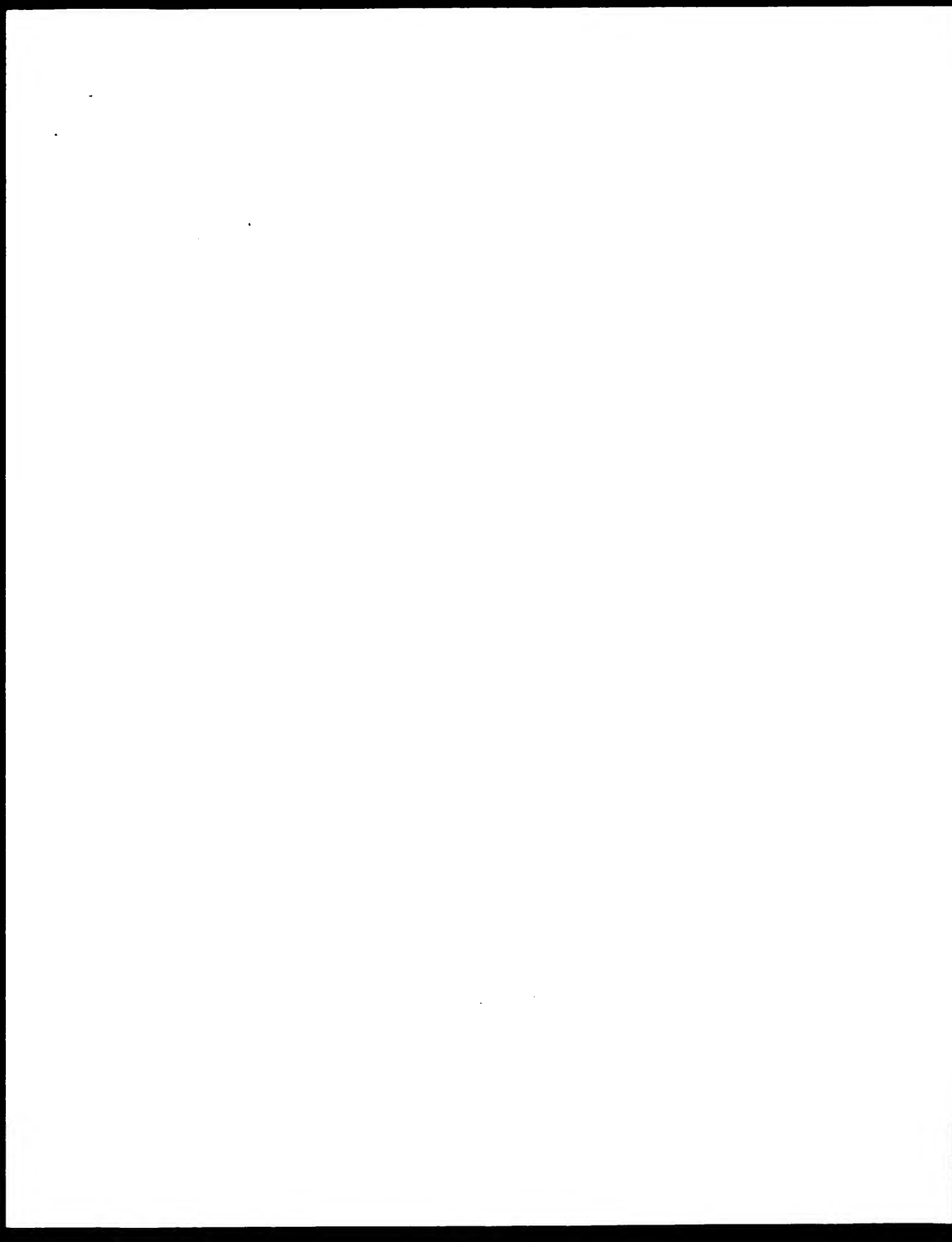
SUMMARY

Result No.	Query Score	Match Length	ID	Description
------------	-------------	--------------	----	-------------

1	1170	100.0	233	20	AAV29928
2	1179	100.0	223	22	AAV327127
3	814	69.6	197	22	AAV94608
4	807	69.6	207	22	AAV94657
5	575	49.1	150	21	AAV43364
6	472	40.3	97	22	AAV55936
7	472	40.3	97	22	AAV57627
8	472	40.3	97	22	AAV57037
9	203.5	17.4	817	19	AAV48101
10	203.5	17.4	817	20	AAV40147
11	203.5	17.4	849	19	AAV48102

[illegible]

	RESULTS
1	
AAV29978	
XX	Reference standard, molecule, 100 AA.
XX	
AV	AAV29978;
XX	
XX	- R V L Y G A S I A L S E T T G)
XX	
XX	human P22 protein (P22 protein domain).
XX	
XX	Human P22 protein (P22 protein domain);
PW	Genetic information disorder; developmental disorder;
AW	Williams syndrome;
XX	
OS	Homo sapiens.
XX	
PN	US9596731 A.
XX	
PD	28-SEP-1999.
XX	
PF	11-SEP-1998; 9808-0151611.
XX	
PR	11-SEP-1998; 9808-0151611.
XX	
PA	(INCYT) INCYTE PHARM INC.
XX	
R1	The H. Patterson Co., Au Young J.
XX	
DE	WPt, 1999 561035/47.
XX	
XX	N STR, AAV21259.
XX	
XX	Molecular analysis screening cellular junction P22 protein domains useful for
PT	the prevention, diagnosis and treatment of disorders associated with
PT	defective cell signaling such as cancers and neurological and



[illegible]

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EM protein - protein search, using sw model

Run on: May 7, 2002, 12:41:28 : Search time 24.52 seconds
(without alignments)
1449.041 bits (1176.911 bits) 0.0130 e/byte

Title: US-09-909-005-1
Port score: 1170
Sequence: 1 MKRVEVAVMAACTIV
1170:XXXXXXXXXXXXXXXXXXXX

Scoring table:
BLOSUM62
Gapop 10.0, expect 0.5

Searched: 473505 seqs, 1627239 residues
Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post processing: Minimum Match: 0%
Maximum Match: 100%
Listing first 45 summaries

Database: SPTRMBL_17:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_molt:
8: sp_oranella:
9: sp_phage:
10: sp_plant:
11: sp_protist:
12: sp_vertebrate:
13: sp_vertebrate:
14: sp_unclassified:

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

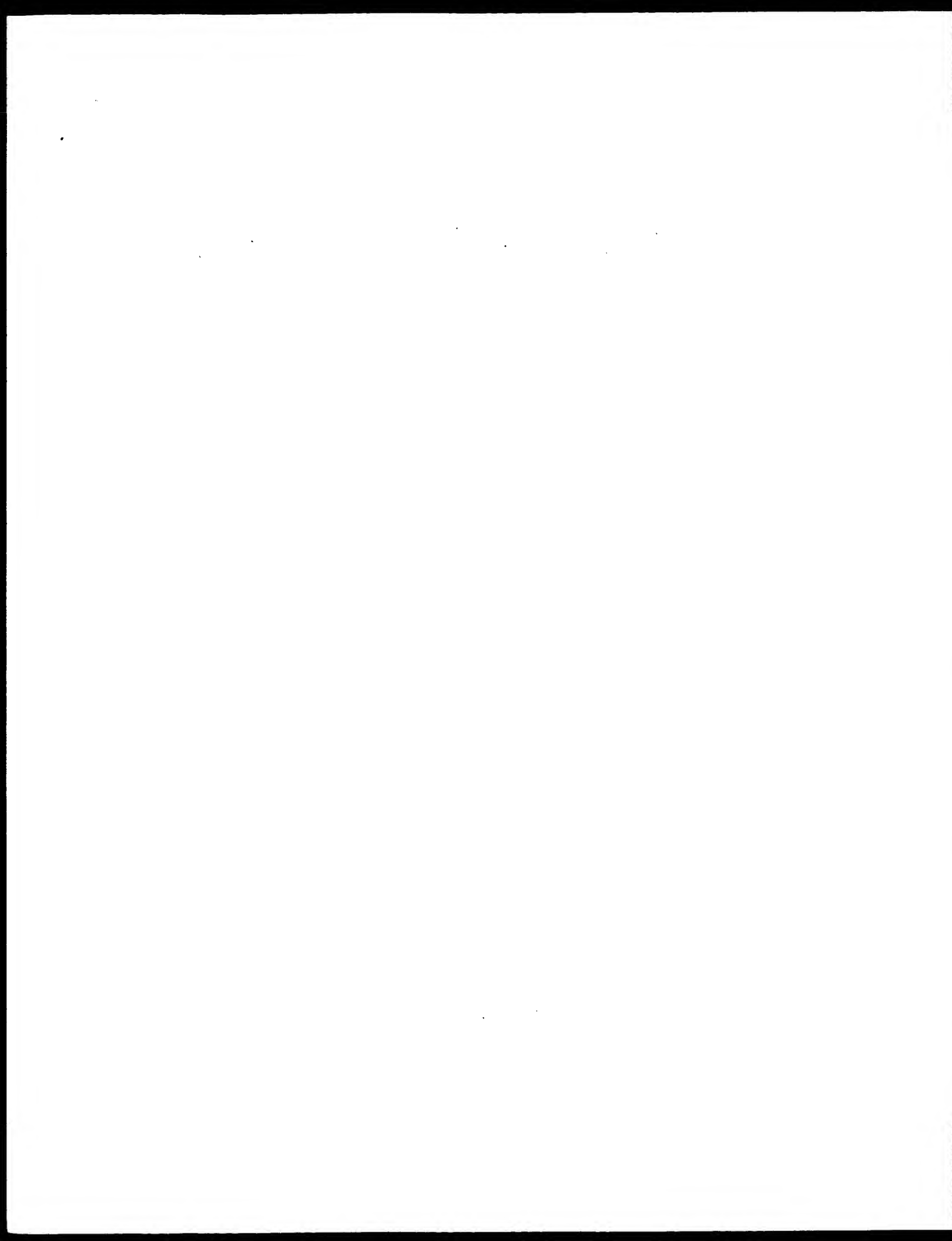
SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1170	100.0	233	4	Q14910 Homo sapien
2	1077.5	92.1	219	11	Q97250 67/266 ratios nerv
3	814	69.6	197	4	Q9N039 Oryzops homo sapien
4	814	69.6	197	11	Q88952 mus musculu
5	809	69.1	207	11	Q92252 ratios nerv
6	809	69.1	207	11	Q88951 mus musculu
7	807	69.0	207	4	Q9H856 20046 homo sapien
8	799	68.3	234	11	Q90291 994291 mus musculu
9	758	61.3	182	11	Q92251 67/266 ratios nerv
10	754	64.1	195	5	Q9V087 69437 drosophila
11	662	56.6	317	5	Q9V036 69437 drosophila
12	648.5	55.4	171	5	Q17458 017458 schistosoma
13	643.5	55.0	297	5	P99976 099976 caenorhabdi
14	233.5	20.0	967	5	Q9H179 09H179 caenorhabdi
15	233.5	20.0	1064	5	Q18165 018165 caenorhabdi
16	208.5	17.8	960	5	Q9VY25 09VY25 drosophila
17	199.5	17.1	455	11	Q9E111 09E111 mus musculu
18	198.5	17.3	462	4	Q9H026 69436 homo sapien
19	191.5	16.4	205	11	Q9E1K3 69E1K3 mus musculu

20	187.5	16.0	526	11	Q08783 008783 mus musculu
21	186.5	15.9	2854	11	Q51454 051454 ratios nerv
22	185	15.8	927	11	Q62492 062492 mus musculu
23	177	15.1	1012	5	Q21075 021075 caenorhabdi
24	176.5	15.1	2484	6	Q28006 028006 bos taurus
25	176	15.0	431	5	Q19846 019846 caenorhabdi
26	174.5	14.9	453	4	Q43798 043798 homo sapien
27	174.5	14.9	2943	4	Q75920 075920 homo sapien
28	173.5	14.8	2460	11	Q64512 064512 mus musculu
29	172.5	14.7	176	5	Q9V087 69437 drosophila
30	170.5	14.6	140	11	Q9C269 09C269 mus musculu
31	167.5	14.3	126	11	Q62370 062370 mus musculu
32	167	14.3	1031	4	Q9H557 09H557 homo sapien
33	167	14.3	1264	4	Q9H556 09H556 homo sapien
34	167	14.3	1353	4	Q9H558 09H558 homo sapien
35	166.5	14.2	140	4	Q9P001 09P001 homo sapien
36	166	14.2	499	4	Q9H559 09H559 homo sapien
37	165	14.1	1171	11	Q54893 054893 mus musculu
38	165	14.1	1256	4	Q75085 075085 homo sapien
39	164	14.0	1524	4	Q15249 015249 homo sapien
40	164	14.0	1552	4	Q60843 060843 homo sapien
41	164	14.0	1582	4	Q43742 043742 homo sapien
42	164	13.8	1551	4	Q14160 014160 homo sapien
43	161.5	13.8	1332	11	Q9V082 09V082 mus musculu
44	161	13.8	1337	11	Q92430 092430 ratios nerv
45	160	13.7	267	4	Q9H034 69H034 homo sapien

ALIGNMENTS

RESULT 1
ID 014910 PRELIMINARY: PRT: 233 AA.
AC 014910:
DT 01-JAN-1998 (TrEMBL: 05, Created)
DT 01-MAY-1999 (TrEMBL: 10, Last sequence update)
DT 01-JUN-2001 (TrEMBL: 17, Last annotation update)
DE VELL 1 (TAX INTERACTION PROTEIN 33) (FRAGMENT).
GN MALS-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SUBMITTER FROM N.A.
RC HSSRP TESTIS.
EX HSSRP: 98421216, PubMed 9753324;
RA Butz S., Okamoto M., Studot T.C.;
RT "A tripartite protein complex with the potential to couple synaptin
KL cell cycle exocytosis to cell adhesion in brain."
RN [2]
RP SOURCE OF 32-233 FROM N.A.
RA Kousset R., Fature S., Bastians C., Bantianos P., Adnot P.;
RC "Sequence 1610-0(1997)."
RN [3]
RP SUBMITTER FROM N.A.
RC HSSRP: 98421221, PubMed 9941234;
RA De K., Barth R., Li M., Brodt D.S.;
RT "LIN-7 homologs clustered at brain synapses in association with the
FL F-actin complex of nestin-7 (NCAM-140(1999))."
FL HBB: A098763, A078481;
DR EMBL: A098763, A078481;
DR EMBL: A173881, A048500;
DR HSSRP: Q12923, 992;
DR Interpro: IPR001478; P02;
DR Pfam: PF00795; P02; 1;
DR SMART: SM00226; P02; 1;
DR PROSITE: PS00106, P02; 1;
FT REGION: 1..1




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DR Pfam: PF00625; Guanylate_Kin. 1.
DR Pfam: PF00595; ED2. 3.
DR Pfam: PF00018; SH3. 1.
DR SMART: SM00072; GUKC. 1.
DR SMART: SM00228; PDZ. 3.
DR SMART: SM00426; SH3. 1.
DR PROSITE: PS00856; GUANYLATE_KINASE_1. 1.
DR PROSITE: PS00552; GUANYLATE_KINASE_2. 1.
DR PROSITE: PS00106; PDZ. 3.
DR PROSITE: PS00002; SH3. 1.
KW SH3 domain; Repeat.
FT DOMAIN 98
FT DOMAIN 184
FT DOMAIN 193
FT DOMAIN 279
FT DOMAIN 421
FT DOMAIN 501
FT DOMAIN 536
FT DOMAIN 606
FT DOMAIN 662
FT DOMAIN 852
FT CONFLICT 181
FT CONFLICT 228
FT CONFLICT 326
FT CONFLICT 339
FT CONFLICT 349
FT CONFLICT 450
FT CONFLICT 464
FT CONFLICT 474
FT CONFLICT 476
FT CONFLICT 478
FT CONFLICT 484
FT CONFLICT 506
FT CONFLICT 569
FT CONFLICT 586
FT CONFLICT 626
FT CONFLICT 639
FT CONFLICT 726
FT CONFLICT 733
FT CONFLICT 749
FT CONFLICT 756
FT CONFLICT 793
FT CONFLICT 794
SQ SEQUENCE 852 AA: 94934 MW: 18014ABSGFSE09 CPG64;

Query Match 18.7% Score 219, E-1, Length 823,
Post Local Similarity 35.7% Pred. No. 1.5e-08
Matches 51; Conservative 24; Mismatches 54; Indels 14; Gaps 2.

UY 88 AIAKAVAAAFASGSHRRPVVETPTREGLFNVWYCFQNSVYISPTTCVAERIG 147
Db 401 ATRPSTVTLQFALSLDEGRPKVVIHKSGDELSENIWQ3-EDRGTFVSLACGADISG 459
UY 148 GIKKQDLISVNVSVGFGRHFRKAVHIVAKTSVLLVVRVYVYVYVYVYVYVYVYV 204
Db 460 HIGRQDILSVNITVPGASHEDAAALAKGAGQVITIIAGYQPDYAPFAKIHDLRDM 519
UY 205 -----TAKRQDQQLDQ 217
Db 520 MNSMSGSGSGSLPTNCKPSLYV 542

RESULT 2
DIAG_HUMAN STANDARD; PRT: 870 AA.
AC Q15700;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-APR-2001 (Rel. 40, Last annotation update)
DE CHANNEL ASSOCIATED PROTEIN OF SYNAPSE-110 (CHAPSIN-110) (DISCS, LARGE
DE HOMOLOG 2).
DE DIAG2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NBI_TaxID:9606;
KN [1]
KP SEQUENCE FROM N.A.

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FX MEDLINE:96310881; PubMed:8755482;
RA Kim P., Cho K.-O., Rothschild A., Sheng M.;
FT "heteromultimerization and NMDA receptor-clustering activity of
FT Chapsyn-110, a member of the PSD-95 family of proteins."
AL Neuron 17:105-113(1996).
CC 1 FUNCTION: INTERACTS WITH THE CYTOPLASMIC TAIL OF NMDA RECEPTOR
CC SUBUNITS AS WELL AS POSTION CHANNELS.
CC 1 SIMILARITY: CONTAINS 3 PDZ/DHR DOMAINS.
CC 1 SIMILARITY: CONTAINS 1 SH3 DOMAIN.
CC 1 SIMILARITY: BELONGS TO THE MAGUK FAMILY OF CELL JUNCTION PROTEINS.
CC 1 SIMILARITY: BELONGS TO THE MAGUK FAMILY OF CELL JUNCTION PROTEINS.
CC This SWISS-Prot entry is copyright. It is produced through a collaboration
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CC entities requires a license agreement (see http://www.isb-sib.ch/announcements
CC or send an email to license@sib.ch).
DR IMGT: 033375; AAB94912.1.
DR HSPG_Q12959; IPDR.
DR MIM: 603583; -.
DR InterPro: IPR000619; Guanylate_Kin.
DR InterPro: IPR001478; PDZ.
DR InterPro: IPR001452; SH3.
DR Pfam: PF00625; Guanylate_Kin. 1.
DR Pfam: PF00595; PDZ. 3.
DR Pfam: PF00018; SH3. 1.
DR SMART: SM00072; GUKC. 1.
DR SMART: SM00228; PDZ. 3.
DR SMART: SM00426; SH3. 1.
DR PROSITE: PS00856; GUANYLATE_KINASE_1. 1.
DR PROSITE: PS00552; GUANYLATE_KINASE_2. 1.
DR PROSITE: PS00106; PDZ. 3.
DR PROSITE: PS00002; SH3. 1.
KW SH3 domain; Repeat.
FT DOMAIN 98
FT DOMAIN 184
FT DOMAIN 193
FT DOMAIN 279
FT DOMAIN 421
FT DOMAIN 501
FT DOMAIN 536
FT DOMAIN 606
FT DOMAIN 662
FT DOMAIN 852
SQ SEQUENCE 870 AA: 97500 MW: 89640A0G19P0F59 CPG64;

Query Match 18.5% Score 217.5; DB 1; Length 870;
Post Local Similarity 29.3% Pred. No. 2e-08
Matches 55; Conservative 31; Mismatches 59; Indels 43; Gaps 4;

UY 43 GYVFAKRLSLKVLQSEFCTAIEVYQYHPTVNVGTEPPAVATVAHVAASEG 102
Db 385 GLIPDSSEMS-----HSQSTATROPSTHGVAVSLG----- 417
UY 103 HSHREVEELKTRDELSTFNVWPKRLASPTTSSVVALEHSLKRLGALVAVKVS 162
Db 418 --EPRKVLHKGSTGLPGLVIGG-EDRGTFVSLACGADISG 474
UY 163 VDFGRHFRKAVHIVAKTSVLLVVRVYVYVYVYVYVYVYVYVYVYVYVYVYVYVY 209
Db 475 IRTASHHQAALAKGAGQVITIIAGYQPDYAPFAKIHDLRDMNMSMSGSGSLPTN 534
UY 210 QQQQQLDQ 217
Db 535 QKSTAVK 542

RESULT 3
DIAG_DROME STANDARD; PRT: 900 AA.
AC P31007;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)

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DE LETHAL(DISC) LARGE-1 TUMOR SUPPRESSOR PROTEIN
GN 1431.
CS Drosophila melanogaster (Fruit fly).
CS Eukaryota; Metazoa; Arthropoda; Insecta; Hexapoda; Insecta;
CS Preyoptera; Neoptera; Endopterygota; Diptera; Brachycera; Mescomorpha;
CS Ephydridae; Prosoptidae; Prosoptini;
CS Nhl_taxid=7227;
KN 111
KN SEQUENCE FROM N.A.
KA MEDLINE=9130294; PubMed=1651169;
KA Woods D.F., Bryant P.J.;
KT "the discs large tumor suppressor gene of Drosophila encodes a
KT quynylate kinase homolog localized at septate junctions.";
KL J Cell Biol 66:451-464(1991).
CS -1 FUNCTION: LOSS OF THIS PROTEIN CAUSES LARGE IMAGINAL DISKS BY
CS ALLOWING NEOPLASTIC GROWTH. THE PRESENCE OF A GUANYLATE KINASE
CS DOMAIN SUGGESTS INVOLVEMENT IN APPROPRIATE CELLULAR ADHESION AS WELL
CS AS SIGNAL TRANSDUCTION TO CONTROL CELLULAR PROLIFERATION. THE DLG
CS PROTEIN PLAYS A CRITICAL ROLE AT SEPTATE JUNCTIONS IN CELLULAR
CS GROWTH CONTROL DURING LAPAL DEVELOPMENT.
CS -1 SUBCELLULAR LOCATION: CYTOSKELETON-ASSOCIATED. LOCATED AT THE
CS CYTOSOLIC FACE OF THE MEMBRANE IN THE CELLULAR BLAST-DESM AND
CS BERMES ASSOCIATED WITH SEPTATE JUNCTIONS WHICH BEGIN TO FORM
CS BETWEEN EPITHELIAL CELLS AT THE TIME OF DORSAL CLOSURE. IN ADULT
CS FLIES, LOCATED AT THE APICAL-LATERAL MEMBRANE BOUNDARY OF
CS EPITHELIAL CELLS.
CS -1 ALTERNATIVE PRODUCTS: LEADS TO DIFFERENT FORMS OF THE PROTEIN,
CS THE SEQUENCE SHOWN REFERS TO THE PUG-A PROTEIN, THAT IS MOST
CS ABUNDANTLY EXPRESSED.
CS -1 TISSUE SPECIFICITY: BROAD SPECIFICITY. ABUNDANTLY EXPRESSED IN
CS EPITHELIAL TISSUES. DEVELOPMENTAL STAGE DEPENDENT EXPRESSION.
CS -1 SIMILARITY: CONTAINS 3 PDZ/DH DOMAINS.
CS -1 SIMILARITY: CONTAINS 1 SH3 DOMAIN.
CS -1 SIMILARITY: CONTAINS A GUANYLATE KINASE-LIKE DOMAIN.
CS -1 SIMILARITY: BELONGS TO THE MAMKIN FAMILY OF COT1 JUNCTION PROTEINS.
CN
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CN
DR EMBL: M73529; AAA28468.1; -
DR PIR: A39651; A39651.
DR HSP: g17664; lrp.
DR FlyBase: Fbm0001624; dlgl.
DR InterPro: IPR006619; Guanylate_kin.
DR InterPro: IPR001478; PDZ.
DR InterPro: IPR001452; SH3.
DR Pfam: PF006625; Guanylate_kin; 1.
DR Pfam: PF00915; puz; 1.
DR Pfam: PF00018; SH3; 1.
DR SMART: SM0072; GUK; 1.
DR SMART: SM00229; PDZ; 3.
DR SMART: SM00326; SH3; 1.
DR PROSITE: PS00859; GUANYLATE_KINASE_1; 1.
DR PROSITE: PS00052; GUANYLATE_KINASE_2; 1.
DR PROSITE: PS0106; PDZ; 3.
DR PROSITE: PS50002; SH3; 1.
DR Transducer: SH3 domain; Alternative splicing: Repeat.
KW DOMAIN
FT 1 40 126 PDZ 1.
FT 1 154 243 PDZ 2.
FT 1 486 566 PDZ 3.
FT 1 600 670 SH3
FT 1 768 960 GUANYLATE_KINASE.
FT 1 102468 MM: BF87AM262P1BEAD5 C664;
SEQUENCE

Query Match	17.8%;	Score	208.5;	IB	1;	Length	967;
Best Local Similarity	39.3%;	Pred. No.	1e-07;				
Matches	46;	Conservative	49;	Indels	1;	Gaps	1

```

0Y      88 ATAAAGVAAAASASHSHREPVAVLPTETEDALITNWKSEKNSPYTAKRIINQVALNRG 147
DB      466 AVFHTDPAVSIFPHTPEPTITLKGGCGCPFNIVGS-FEGGLGVYSFLADQMLNTS 524
C       118 TFFFTVGLTVRVNVSTHTEFAVLLEAAILSRKVLTVEEIVILLRDLAEALKE 274
DB      525 ELKGDELISVNVMNLTHAIHEFAVAALKTSQVVLLIADVPPEYNMFARIDELK 981
RESULT 4
DLOG_HUMAN STANDARD: PRI: 817 AA.
AC Q92796; Q9U1B;
DT 01-NOV-1997 (Ref. 35, Created)
DT 31-NOV-1997 (Ref. 35, last sequence update)
DT 20-AUG-2001 (Ref. 40, last annotation update)
DE PEPSYANINIC PROTEIN SAPIET (SYNASE-ASSOCIATED PROTEIN 102)
DC (NEUROGENIC FACTOR-DIG) (NE DUS) (OLIGO) (LARGE HOMOLOG 3).
GN LUS3 OR KIAA1232.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RC SEQUENCE FROM N.A.
KC TISSUE=Fetal brain;
EX MEDLINE: 9732623; PubMed-9188857;
RA Mathe V., Prochazka H., Musur J., Nishiyama Y., Morisaki T.,
RA Sasakl T., Nakao M., Kuwano A., Nakagawa M., Usuki Y., Saya H.;
RT "Cloning and characterization of NE-dlg, a novel human homolog of the
RT Drosophila discs large (dlg) tumor suppressor protein interacts with
RL the APC protein.";
RL cdcgene 14:2425-2433(1997).
KH 121
RP SEQUENCE OF 330-817 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=20039619; PubMed-10574462;
RA Nagase T., Ishikawa K.-I., Kikuno K., Hirotsawa M., Nomura N.,
RA Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes XV.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 6:337-345(1999).
CC -1- FUNCTION: INTERACTS WITH THE CYTOPLASMIC TAIL OF THE NMJ RECEPTOR
CC -1- SUBUNIT NR2B (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 3 POU/DZF DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
CC -1- SIMILARITY: CONTAINS A GUANYLATE KINASE-LIKE DOMAIN.
CC -----
CC THIS SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation at
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isdb.ch/eurocenter
CC or send an email to license@isb-sib.ch).
CC
DR EMBL: U49089; AAB61453.1; .
DR EMBL: AB033058; BAA86546.1; .
DR HSPP: Q12959; IPDR.
DR MIM: 300189; .
DR InterPro: IPR000619; Guanylate_kin_1.
DR InterPro: IPR001478; PDZ.
DR Pfam: PF006425; Guanylate_kin_1.
DR Pfam: PF005955; PDZ_3.
DR Pfam: PF000181; SH3_1.
DR SMART: SM000723; GUKCT_1.
DR SMART: SM00228; TRTZ_3.
DR SMART: SM00326; SH3_1.
DR PROFILE: PS00856; GUANYLATE_KINASE_[1].

```


KA Adams L.D., Wong J., Schmitt J.M.
 KL Submitted (Nov 1996) to the EMBL/Genbank/Trna databases.
 KN [4]
 KO X-RAY CRYSTALLOGRAPHY (1.62 ANGSTROMS) OF 402-402.
 KX MEDLINE 96270509; PubMed 8674113;
 KY Doyle J.A., Lee A., Low S.J., Kim E., Sheng M., Mackinnon R.
 R1 Crystal structures of a complexed and peptide-free membrane protein-
 R1 binding domain: molecular basis of P/Q-type recognition by P/Q.
 RL Cell 85:1067-1076 (1996)
 CC -1- FUNCTION: INTERACTS WITH THE CYTOSOLIC TAIL OF NMDA RECEPTOR
 SUBUNIT5. MAY BE INVOLVED IN SYNAPTIC JUNCTIONS PRIMARILY
 ON THE PRESYNAPTIC SIDE (WAS ORIGINALLY THOUGHT TO BE
 POSTSYNAPTIC).
 CC -1- TISSUE SPECIFICITY: PRESYNAPTIC DENSITY FRACTION OF BRAIN.
 CC -1- SIMILARITY: CONTAINS 3 PDZ/DHR DOMAINS.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE MAGOR FAMILY OF CELL JUNCTION PROTEINS.
 CC -----
 CC THIS SWISS-PROT entry is copyrighted. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb.slb.ch/monomer/>
 CC or send an email to license@slb.slb.ch).
 CC -----
 DR EMBL: M96853; AAA01971.1;
 DR EMBL: X6474; CAA07104.1;
 DR EMBL: 072090; AAB9270.1;
 DR PIR: S2497; S2497;
 DR PIR: JH0800; JH0800;
 DR PDB: 1HE9; 2I-ECT-98;
 DR PDB: 1HTE; 2I-ECT-98;
 DR InterPro: IP000619; Guanylate_kin.
 DR InterPro: IP001478; PDZ;
 DR InterPro: IP001452; SH3;
 DR Pfam: PF00625; Guanylate_kin_1;
 DR Pfam: PF00195; PDZ_3;
 DR Pfam: PF00181; SH3_1;
 DR SMART: SM00722; GORC_1;
 DR SMART: SM00228; PDZ_3;
 DR SMART: SM00426; SH3_1;
 DR PROSITE: PS00856; GUANYLATE_KINASE_1; 1;
 DR PROSITE: PS00852; GUANYLATE_KINASE_2; 1;
 DR PROSITE: PS01061; PDZ_3;
 DR PROSITE: PS00921; SH3_1;
 KW SH3 domain; Repeat; 3D-structure;
 FT DOMAIN 65..151 FIC 1;
 FT DOMAIN 160..246 FIC 2;
 FT DOMAIN 113..393 SH3;
 FT DOMAIN 428..498 SH3;
 FT DOMAIN 534..724 GUANYLATE_KINASE;
 FT DOMAIN 61..61 M -> L (IN REF. 2);
 FT CONFLICT 78..79 S -> I (IN REF. 2);
 FT CONFLICT 177..182 OVERALL -> A (IN REF. 2);
 FT CONFLICT 209..230 A -> S (IN REF. 2);
 FT CONFLICT 254..254 S -> I (IN REF. 2);
 FT CONFLICT 539..555 HLEPKRMANILSEF -> ISLEPKRVTPLTISNNS
 FT CONFLICT (IN REF. 2);
 FT CONFLICT GRI -> R (IN REF. 3);
 FT CONFLICT 623..625 GRI -> R (IN REF. 3);
 SQ SEQUENCE 724 AA; 83465 MW; 792234480P9AD85 CR664;

Query Match 16.8% Score 196.5; DB 1; Length 724;
 Post Local Similarity 41.4%; Prev. Neg. 5.4e-07;
 Matches 41; Conservative 19; Mismatches 38; Indels 1; Gaps 1;

57 100 EVVLLPRTTGVVDMPTDSTVYVLTGVNADHSDGSGVAVSRVSGVLC 195
 DB 411 PRKLVHDSGDSGDSVAVFVDFGDSFVAVFVAVLSSTPRKGVTSNVDLEN 469

57 176 LTRFVAVSLKALMSKLVSTVTPVLLMADLFLR 204
 DB 470 ASHQAALAKKNAGVYVITIAOTKREYSFPAKTIIDLR 408
 RESULT 9
 LE64 HUMAN
 LE 3524 J0923; STAH/AFD; FET; 767 AA.
 AC P29452; C92941; G00KKB;
 DT 01-NOV-1997 (ref: 35, created)
 FT 10-EAY-2000 (ref: 39, last sequence update)
 LE 20-AUG-2001 (ref: 40, last annotation update)
 LE Presynaptic density protein 95 (psd95) (human, clone H-mem-4).
 GN D104 OR PSD95.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Tissue: testis; gland;
 EX MEDLINE 9743292; PubMed 926732;
 FA STELLINGSMA D.C., BLOK J.E., YON J., BRYANT P.J.
 FT "Human postsynaptic density-95 (psd95): location of the gene (D10S4)
 FT and possible function in neuronal as well as in neural tissues."?
 FL Genomics 44:192(1997)
 RN [2]
 RP REVISIONS.
 RC Tissue: Mammary gland;
 RA Stathakis D.C., BLOK J.E., YON J., BRYANT P.J.
 RL Submitted (Oct 1998) to the EMBL/Genbank/Trna databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC MEDLINE 20047407; PubMed 10582582;
 RA STELLINGSMA D.C., BLOK J.E., YON J., BRYANT P.J.,
 RA Small K., BOGGSAN S., SAUNDEN O., ANDREWS S., BRYANT P.J.
 FT "Genomic organization of human D104, the gene encoding postsynaptic
 FT density 95."?
 FL Genomics 44:2250-2255(1999).
 RN [4]
 RP SEQUENCE OF 81-401 FROM N.A.
 RC Tissue: brain;
 RA BRENNAN J.E., BLOK J.E., PARLSON J.F., MANADA W.F., MCELROY J.A.;
 RL Submitted (Aug 1996) to the EMBL/Genbank/Trna databases.
 CC -1- FUNCTION: INTERACTS WITH THE CYTOSOLIC TAIL OF NMDA RECEPTOR
 CC SUBUNIT5. MAY BE INVOLVED IN SYNAPTIC JUNCTIONS PRIMARILY
 CC ON THE PRESYNAPTIC SIDE (WAS ORIGINALLY THOUGHT TO BE
 CC POSTSYNAPTIC).
 CC -1- TISSUE SPECIFICITY: PRESYNAPTIC DENSITY FRACTION OF BRAIN.
 CC -1- SIMILARITY: CONTAINS 3 PDZ/DHR DOMAINS.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE MAGOR FAMILY OF CELL JUNCTION PROTEINS.
 CC -----
 CC THIS SWISS-PROT entry is copyrighted. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@slb.slb.ch).
 CC -----
 DR EMBL: U8192; AAC52113.1;
 DR EMBL: AF156495; AAB56173.1;
 DR EMBL: U8138; AAB07736.1;
 DR EMBL: Q12959; IPRK;
 DR MIM: 602887;
 DR InterPro: IP000619; Guanylate_kin.
 DR InterPro: IP001478; PDZ;
 DR InterPro: IP001452; SH3;
 DR Pfam: PF00625; Guanylate_kin_1;
 DR Pfam: PF00195; PDZ_3;

between the Swiss Institute of Bioinformatics and the EMBL, at the European Bioinformatics Institute. There are no restrictions

RT "molecular interaction and spatial distribution of SAP90, a novel presynaptic protein homologous to SAP90 and the lipophilic discs-large tumor suppressor protein."

RESULT 14

IL16_HUMAN STANDARD: PRT: 631 AA.

AC 014005: Q16435; Q00P18;

DE 01-NOV-1997 (Ref. 35, Created)

DE 30-MAY-2000 (Ref. 39, Last sequence update)

DE 20-AUG-2001 (Ref. 40, Last annotation update)

DE INTERLEUKIN-16 PRECURSOR (IL-16) (LYMPHOCYTE CHIMATRACTANT FACTOR) (IL-16).

GN IL16.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

OX NCBI_Taxid 9606;

RN [1]

RP SEQUENCE FROM N.A.

RA TISSUE: Peritoneal blood.

RA Kozieci J.H.

PL Submitted (JAN 1999) to the EMBL/GenBank/DBJ databases.

PN [3]

PP SEQUENCE FROM N.A.

RA MEDLINE:99145586; PubMed 9990060;

RA Bannett N., Avots A., Baier M., Serfling E., Kurth R.;

PT "CA-binding protein factors, in concert with the covalent CCR binding protein, control the induction of the interleukin 16 promoter in T lymphocytes";

PL Proc Natl Acad Sci U S A 96:1541-1546(1999).

RN [4]

RP SEQUENCE OF 241-631 FROM N.A.

RA MEDLINE:96211111; PubMed 8609994;

RA Bannett N., Baier M., Werner A., Kurth R.;

PT "Interleukin-16 or not?";

PL Nature 381:30-30(1996).

RN [4]

RP SEQUENCE OF 502-631 FROM N.A.

RA TISSUE: Peritoneal blood;

RA MEDLINE:94255490; PubMed 791097;

RA Grisham W.W., Gubler E.M., Blaser N., W.M., Nakke F.;

PT "Molecular and functional analysis of a lymphocyte chemoattractant factor: association of biologic function with CD4 expression";

PL Proc Natl Acad Sci U S A 91:5109-5113(1994).

RN [4]

RP SEQUENCE OF 502-631 FROM N.A.

RA Du Y., Du G.X., Hou L.H., Wang H.T.;

PT "cDNA sequence of interleukin-16 cloned from human PBs";

PL Submitted (MAR 1998) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: STIMULATES A MIGRATORY RESPONSE IN CD4+ LYMPHOCYTES, MONOCYTES, AND EOSINOPHILS. ALSO INDUCES T-LYMPHOCYTE EXPRESSION OF INTERFERON 2 PERCEPTOR 1 CD40 FOR CD4

CC -1- SUBUNIT: HOMOTETRAMER

CC -1- SIMILARITY: CONTAINS 2 PPTZ/DHR DOMAINS.

CC

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CC

DR EMBL: M90391; AAD04636.1;

DR EMBL: AF072811; AA15990.1;

DR EMBL: S81631; AAR3271.2;

DR EMBL: AF053412; AAC12442.1;

DR HSSP: Q12959; IPDR.

DR MIM: 603035;

DR RefSeq: NP001478; PDR.

DR RefSeq: P00095; PDR.

DR SMART: SMC328; PDR.

DR PROSITE: P50106; PDR: 2.

KM Cytokine; Chemotaxis.

FT PROPER 1 2 631 INTERLEUKIN 16.

FT CHAIN 1 2 631 PPTZ 1.

FT DOMAIN 411 496 PPTZ 2.

FT DOMAIN 533 618 PPTZ 2.

FT CONFLICT 104 104 E-2 D (IN REF. 2).

FT CONFLICT 233 233 E-2 L (IN REF. 2).

FT CONFLICT 241 243 PPTZ (IN REF. 3).

FT CONFLICT 319 319 E-2 A (IN REF. 1).

SO SEQUENCE 631 AA; 66694 MW; 24303670603640 CRC64;

Query Match 13.2% Score 155, DF 1, Length 641;

Host Local Similarity 24.1% Prod No 0.00044;

Matches 53; Conservative 44; Mismatches 70; Indels 44; Gaps 7;

QY 5 SVTSAPLAPMATLVVPPPLLP---IWAFAPIPAFQESGE-----VWVRKUSLK 54

DB 222 STGESMDGAMASAFESALPCELSLSEIPEVTEPITFAVPVTVVHSGIQTGQSVI 381

QY 55 KYQSDHPCVAPVYQYMEETTVRCQPEPRAPATKAT---VAAPASDHSHPVVF 119

DB 382 SLSSSEELKLELVKVIKP-----ATIKQIPIHVTILAKRRG----- 420

QY 111 LFTFELGKLVNMCFF--QNSPTYSFIPPCVAFEPFQIKRQGLISVNVSGVQPHF 164

DB 421 ----ACGLPSLNSGADLEKVTIVHPFNPNTLASQPTTGKGNVISTNRSIKGTTH 475

QY 170 KAVPIIKAKOSKIV---PIPKVLFEMPAPEKIPKA 206

DB 476 DALALPQAEPPQAVIVFKILPAMPPLNSTDSASA 515

RESULT 15

IL25_HUMAN STANDARD: PRT: 145 AA.

AC P57105;

DE 20-AUG-2001 (Ref. 40, Created)

DE 20-AUG-2001 (Ref. 40, Last sequence update)

DE 20-AUG-2001 (Ref. 40, Last annotation update)

DE MITOCHONDRIAL OUTER MEMBRANE PROTEIN 25.

GN OMT25.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

OX NCBI_Taxid 9606;

RN [1]

RP SEQUENCE FROM N.A.

RA TISSUE: Placenta;

RA Isogai T., Goto T., Hayashi K., Sugiyama T., Otsuki T., Suzuki T., Nishiyama M., Nagai K., Sugino S., Shibata A., Sudo H., Wajatsuna M., Hosoki T., Fuku Y., Kodaira H., Kondo H., Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S., Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K., Yamamoto T., Wakamatsu A., Nakamura Y., Nagahata K., Masuko Y., Rikimaru K., Iwakura T.;

PT Submitted (FEB 2000) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: CONTAINS 1 PPTZ/DHR DOMAIN

CC

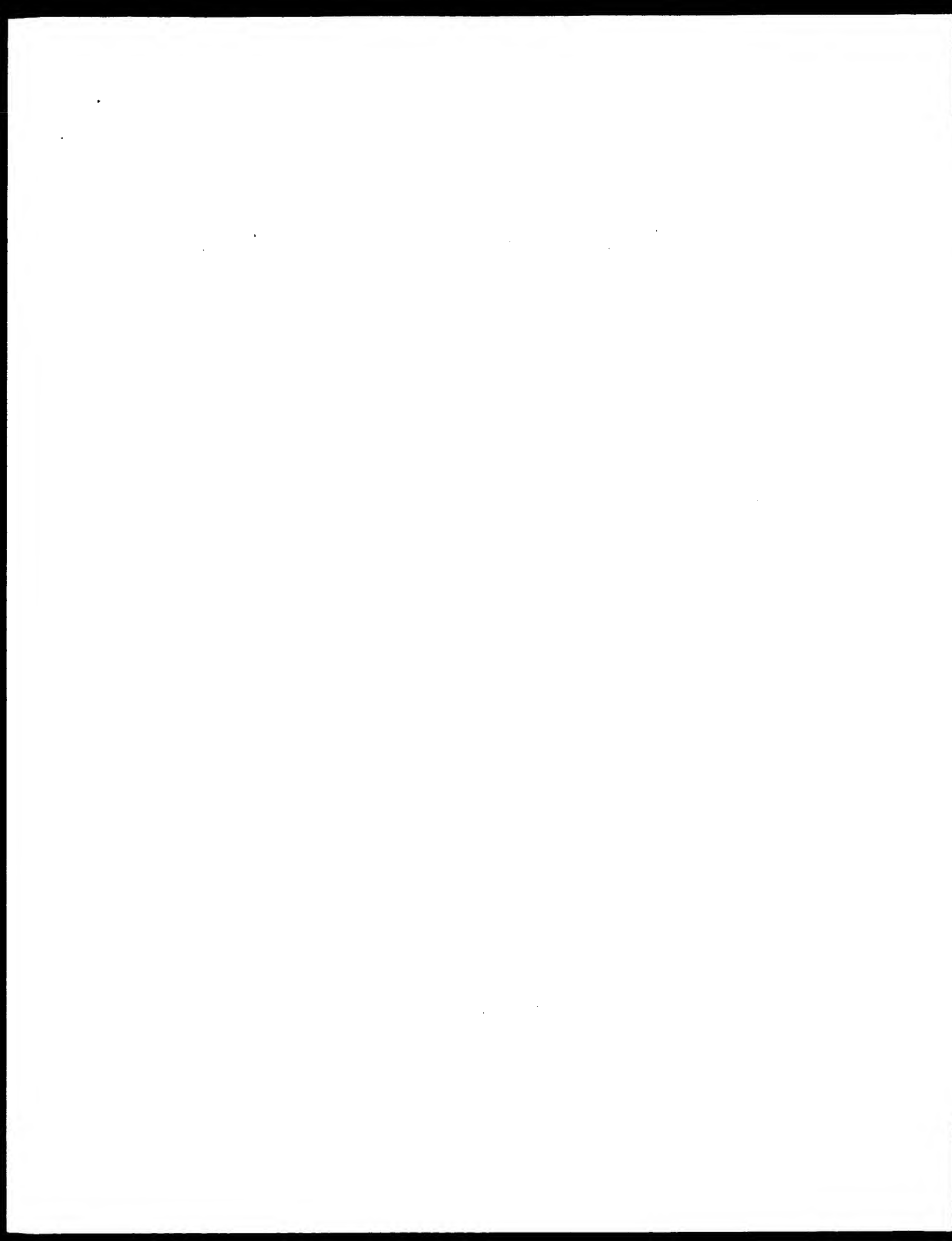
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CC

DR EMBL: AK062133; EAA92998.1;

DR RefSeq: NP001478; PDR.

DR Pfam: PF00757; PDR.



SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/566,291
FILING DATE: 09 AUG 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/115,573
FILING DATE: 01-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
PRACTICE NUMBER: 41 616
REFERENCE/EXEMPT KIT NUMBERS: 1,441,770/99
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/720-4500
TELEFAX: 617/720-2441
FLEX: 94-1742 EZEKIEL
INFORMATION FOR SFO ID NO: 8;
SEQUENCE CHARACTERISTICS:
LENGTH: 2465 amino acids
TYPE: amino acid
POLARITY: linear
MOLECULE TYPE: protein
US-08-566-291-4

Query Match	15.48	Score 180.5	DB 37	Length 2466
Query Local Similarity	27.9%	Ident. No. 5,56	69	
Matches	517	Conservative	643	Indels 37; Gaps 4
QY	22	PLHLLDVAALHLEELNPEVWVHPTSTFVLTSEETALREYVYMMHTLVN	91	
DB	993	PLVVAHVAHSHLSHSTASTASTAVTKINSNV	ASTINPS	1033
QY	82	PEFPAFAIAKAVY	ANFAAEDHSHREYVLLKPT	126
DB	1034	PERKHHSNHSSTHEDPOGAVLVVIAHKNHSIVSTSEKELLVNLKKAAYGLQFQITGG		1093
QY	127	HQ--NSDPIYSRIHEDVAERHDKIKRDEGLISVYVSEVDEHHAAYVLAASAKSYA	184	
DB	1094	KMRIDIAHFIISVAAGGAVADHDELENGDGLISVNSVSLGVSHHATILNNAPETVI	1153	
QY	184	LVV	186	
DB	1154	LVI	1156	

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1      RES011      8
2      PCT-US94-09943-2
3      Sequence 2: Application EC/US-40943
4      GENERAL INFORMATION:
5      APPLICANT:
6      APPLICANT:
7      APPLICANT:
8      APPLICANT:
9      APPLICANT:
10     APPLICANT:
11     APPLICANT:
12     TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL
13     TITLE OF INVENTION: EXPRESSION OF NOVELTY SEQUENCES FOR NOVEL PROTEIN
14     TITLE OF INVENTION: TYROSINE PHOSPHATASES
15     NUMBER OF SEQUENCES: 4
16     CORRESPONDENCE ADDRESS:
17     STREET: 600 ATLANTIC AVENUE
18     CITY: BOSTON
19     STATE: MASSACHUSETTS
20     COUNTRY: USA
21     COMPUTER READABLE FORM:
22     MEDIUM TYPE: FLOPPY disk
23     COMPUTER: IBM PC compatible
24     OPERATING SYSTEM: PC DOS MS DOS
25     SOFTWARE: Patent Release #1.0, Version #1.25
26     CURRENT APPLICATION DATA:
27     APPLICATION NUMBER: PCT/US94/09943
28     FILING DATE: 01-SEP-1994
29     CLASSIFICATION:
30     PRIOR APPLICATION DATA:
31     APPLICATION NUMBER: US 08/715,573
32     FILING DATE: 01-SEP-1994
33     ATTORNEY/AGENT INFORMATION:
34     NAME: TWOMEY, MICHAEL, J.
35     REGISTRATION NUMBER: P-48,479
36     REFERENCE/EXCIT NUMBER: 1,467,720W
37     TELECOMMUNICATION INFORMATION:
38     TELEPHONE: 617/720-3500
39     TELEFAX: 617/720-2441
40     FAX: 92-1742 EXTENDED
41     INFORMATION FOR SEQ ID NO: 2:
42     SEQUENCE CHARACTERISTICS:
43     LENGTH: 2466 amino acids
44     TYPE: amino acid
45     TOPOLOGY: linear
46     MOLECULE TYPE: protein
47     PCT-US94-09943-2

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Query Match	15.48;	Score 180.5;	DB 5;	Length 2466;
Host/Local Similarity	27.98;	Pred. No. 5.50	09,	
Matches	51;	Conservative	41;	Mismatches 64,
				Indels 37,
				Gaps 4

[illegible]

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1  RESULT 9
2  US-09-106-998-4
3  : Sequence 3, Application US/09106998
4  : Patient No. 6291173
5  : GENERAL INFORMATION:
6  : APPLICANT: Bartel, Paul L.
7  : APPLICANT: Davila, Sean V.
8  : TITLE OR INVENTION: MSC2: An MMAC1 Interacting Protein
9  : FILE REFERENCE: MSC2
10 : CURRENT APPLICATION NUMBER: US/09/306,998
11 : CURRENT FILING DATE: 1999-05-07
12 : EARLIER APPLICATION NUMBER: US 602084,740
13 : EARLIER FILING DATE: 1998-05-08
14 : NUMBER OF SEQ ID NOS: 72
15 : SOFTWARE: Patent In Ver. 2.0
16 : SEQ ID NO 3
17 : LENGTH: 2017
18 : TYPE: PRT
19 : ORIGIN: Homo sapiens
20 : US-09-106-998-4

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[illegible]

RESULT 10
 US-09-100-804-16
 Section 16, Application 07/3910804
 Patent No. 666472
 GENERAL INFORMATION:
 APPLICANT: SARKIS, JAN
 APPLICANT: SARKIS, JAN
 APPLICANT: CLAESON-WELSH, LENA
 APPLICANT: HELDIN, CARL-HENRIK
 TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL
 TITLE OF INVENTION: EXPRESSION OF NOCTURNAL STRUCTURE FOR N-VIL PROTEIN
 TITLE OF INVENTION: TYROSINE PHOSPHATASES
 NUMBER OF FIGURES: 34
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: WOLF, GREENFIELD & SAKIS, P.C.
 STREET: 600 ATLANTIC AVENUE
 CITY: BOSTON
 STATE: MASSACHUSETTS
 COUNTRY: USA
 ZIP: 02210
 COMPUTER READABLE FORM:

db 5 GLOPNVWG-EDGEGTPISTLAGSPADLSGFLKRGDRIISVNGVDLKNASHQDAIALK 63

UY 177 AAKDSVKIV 185

db 64 NAGQIVTII 72

RESULT 15

US-08-410-804-1

? Sequence 1, Application US/08410804

? Patent No. 5612994

? GENERAL INFORMATION:

? APPLICANT: Reed, John C.

? APPLICANT: Sato, Takaki

? TITLE OF INVENTION: FAS ASSOCIATED PROTEINS

? NUMBER OF SEQUENCES: 22

? CORRESPONDENCE ADDRESS:

? ADDRESSER: Cathryn Campbell

? STREET: 4370 La Jolla Village Drive, Ste 700

? CITY: San Diego

? STATE: California

? COUNTRY: United States

? ZIP: 92122

? COMPUTER READABLE FORM:

? MEDIUM TYPE: Floppy disk

? COMPUTER: IBM PC compatible

? OPERATING SYSTEM: PC-DOS/MS-DOS

? SOFTWARE: Patent in Release #1.0, Version #1.25

? CURRENT APPLICATION DATA:

? APPLICATION NUMBER: US/08/410,804

? FILING DATE: 27-MAR-1995

? CLASSIFICATION: 435

? PRIOR APPLICATION DATA:

? FILING DATE: 14-JUN-1994

? ATTORNEY/AGENT INFORMATION:

? NAME: Campbell, Cathryn

? REGISTRATION NUMBER: 31,815

? REFERENCE/BOOKET NUMBER: P-LJ 1389

? TELECOMMUNICATION INFORMATION:

? TELEPHONE: (619) 535-9001

? TELEFAX: (619) 535-8949

? INFORMATION FOR SEQ ID NO: 1:

? SEQUENCE CHARACTERISTICS:

? LENGTH: 610 amino acids

? TYPE: amino acid

? TOPOLOGY: linear

? MOLECULE TYPE: protein

US-08-410-804-1

Query Match 13.4%; Score 156.5; Dh 1; Length 6.0;

Best Local Similarity 27.4%; Pred. No. 1.9e-07;

Matches 40; Conservative 26; Mismatches 43; Indels 37; Gaps 3;

UY 78 VNCCEPKARAKATVAFAFASGSHPR-----V 108

db 31 ISLVTVSYSPKDSMEGATVSSQWQTPQCFSSSVVTPHPRKPTSSSPFGDIE 90

UY 109 VILPKTDFGDFNV-----MGR---KPNSPVYISPIPGVATPHGAIKRGDLSNG 160

db 91 VFLAKPNSTGISVTVIPIKPCVNTSVYKCTLYVAVIFGCAAEEDPTIKGDVLAWG 150

UY 161 VSEGEHHEKAVELKAADSVKIV 186

db 151 VSLGATHKQAVETLINTGVVHLL 176

Search completed: May 7, 2002, 12:41:41
Job time: 111 sec

